Errors Corrected by the STIC Systems Branch **ENTERED**

Serial Number: 09/612,852

CRF Processing Date: 5/9/2001
Edited by: _____
Verified by: _____ (STIC staff)

RECEIVED
#2 JUN 2 1 2001
6/21
TECH CENTER 1600/290

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as:_____ .

☑ Inserted mandatory headings, specifically: _<1 507 and <1 517_____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1633

```
        RAW SEQUENCE LISTING              DATE: 05/09/2001
        PATENT APPLICATION:  US/09/612,852   TIME: 11:33:32
```

**Does Not Comply
Corrected Diskette Needed**

```
        Input Set : A:\09612852
        Output Set: N:\CRF3\05092001\I612852.raw
```

```
      3 <110> APPLICANT: Curiel, David T.
      4         Krasnykh, Victor N.
      6 <120> TITLE OF INVENTION: Modified Adenovirus Containing A Fiber
      7         Replacement Protein
W-->  8 <130> FILE REFERENCE: D6070CIP
W-->  9 <140> CURRENT APPLICATION NUMBER: US/09/612,852
      9 <141> CURRENT FILING DATE: 2000-07-10
     10 <150> PRIOR APPLICATION NUMBER: US 09/250,580
W--> 11 US 60/074,844
     12 <151> PRIOR FILING DATE: 1999-02-16
W--> 13 1998-02-17
W--> 14 <160> NUMBER OF SEQ ID: 14
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 40
     18 <212> TYPE: DNA
     19 <213> ORGANISM: artificial sequence
W--> 20 <220> FEATURE:
     21 <221> NAME/KEY: primer_bind
     22 <223> OTHER INFORMATION: Forward primer FF.F used to amplify segment of the T4
     23         fibritin gene encoding amino acids Ser-229 through
     24         the carboxy terminal Ala-487.
W--> 25 <400> SEQUENCE: 1
     26 gggaacttga cctcacagaa cgtttatagt cgtttaaatg       40
     28 <210> SEQ ID NO: 2
     29 <211> LENGTH: 37
     30 <212> TYPE: DNA
     31 <213> ORGANISM: artificial sequence
W--> 32 <220> FEATURE:
     33 <221> NAME/KEY: primer_bind
     34 <223> OTHER INFORMATION: Reverse primer FF.R used to amplify segment of the T4
     35         fibritin gene encoding amino acids Ser-229 through
     36         the carboxy terminal Ala-487.
W--> 37 <400> SEQUENCE: 2
     38 aggccatggc caatttttgc cggcgataaa aaggtag           37
     40 <210> SEQ ID NO: 3
     41 <211> LENGTH: 53
     42 <212> TYPE: DNA
     43 <213> ORGANISM: artificial sequence
W--> 44 <220> FEATURE:
W--> 45 <221> NAME/KEY:
     46 <223> OTHER INFORMATION: synthetic oligo, F5._3Swa.T, for the introduction of
     47         SwaI restriction site
W--> 48 <400> SEQUENCE: 3
     49 ttggcccat ttaaatgaat cgtttgtgtt atgtttcaac gtgtttattt ttc     53
     51 <210> SEQ ID NO: 4
     52 <211> LENGTH: 61
     53 <212> TYPE: DNA
```

RAW SEQUENCE LISTING   DATE: 05/09/2001
PATENT APPLICATION: US/09/612,852   TIME: 11:33:32

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Output Set: N:\CRF3\05092001\I612852.raw

```
        54 <213> ORGANISM: artificial sequence
W--> 55 <220> FEATURE:
W--> 56 <221> NAME/KEY:
        57 <223> OTHER INFORMATION: synthetic oligo, F5._3Swa.B, for the introduction of
        58       SwaI restriction site
W--> 59 <400> SEQUENCE: 4
        60 aattgaaaaa taaacacgtt gaaacataac acaaacgatt catttaaatg  50
        61 gggccaatat t                                          61
        63 <210> SEQ ID NO: 5
        64 <211> LENGTH: 57
        65 <212> TYPE: DNA
        66 <213> ORGANISM: artificial sequence
W--> 67 <220> FEATURE:
W--> 68 <221> NAME/KEY:
        69 <223> OTHER INFORMATION: synthetic oligo, FFBBLL.T
W--> 70 <400> SEQUENCE: 5
        71 ggcaggtgga ggcggttcag gcggaggtgg ctctggcggt ggcggatccg  50
        72 gggattt                                               57
        74 <210> SEQ ID NO: 6
        75 <211> LENGTH: 57
        76 <212> TYPE: DNA
        77 <213> ORGANISM: artificial sequence
W--> 78 <220> FEATURE:
W--> 79 <221> NAME/KEY:
        80 <223> OTHER INFORMATION: synthetic oligo, FFBBLL.B
W--> 81 <400> SEQUENCE: 6
        82 aaatccccgg atccgccacc gccagagcca cctccgcctg aaccgcctcc  50
        83 acctgcc                                               57
        85 <210> SEQ ID NO: 7
        86 <211> LENGTH: 36
        87 <212> TYPE: DNA
        88 <213> ORGANISM: artificial sequence
W--> 89 <220> FEATURE:
W--> 90 <221> NAME/KEY:
        91 <223> OTHER INFORMATION: synthetic oligo, RGS6H.T
W--> 92 <400> SEQUENCE: 7
        93 gatctagagg atcgcatcac catcaccatc actaat     36
        95 <210> SEQ ID NO: 8
        96 <211> LENGTH: 32
        97 <212> TYPE: DNA
        98 <213> ORGANISM: artificial sequence
W--> 99 <220> FEATURE:
W--> 100 <221> NAME/KEY:
        101 <223> OTHER INFORMATION: synthetic oligo, RGS6H.B
W--> 102 <400> SEQUENCE: 8
        103 attagtgatg gtgatggtga tgcgatcctc ta      32
        105 <210> SEQ ID NO: 9
        106 <211> LENGTH: 27
        107 <212> TYPE: DNA
```

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                    RAW SEQUENCE LISTING              DATE: 05/09/2001
                    PATENT APPLICATION:  US/09/612,852     TIME: 11:33:32

                    Input Set : A:\09612852
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        108 <213> ORGANISM: artificial sequence
W--> 109 <220> FEATURE:
        110 <221> NAME/KEY: primer_bind
        111 <223> OTHER INFORMATION: primer to PCR amplify FF/6H in pXK.FF/6H
W--> 112 <400> SEQUENCE: 9
        113 ccctcatgaa gcgcgcaaga ccgtctg          27
        115 <210> SEQ ID NO: 10
        116 <211> LENGTH: 27
        117 <212> TYPE: DNA
        118 <213> ORGANISM: artificial sequence
W--> 119 <220> FEATURE:
        120 <221> NAME/KEY: primer_bind
        121 <223> OTHER INFORMATION: primer to PCR amplify FF/6H in pXK.FF/6H
W--> 122 <400> SEQUENCE: 10
        123 cccaagctta gtgatggtga tggtgat        27
        125 <210> SEQ ID NO: 11
        126 <211> LENGTH: 8
        127 <212> TYPE: PRT
        128 <213> ORGANISM: Adenovirus type 5
W--> 129 <220> FEATURE:
        130 <221> NAME/KEY: DOMAIN
        131 <223> OTHER INFORMATION: the beginning of the third pseudorepeat of the
        132       fiber shaft domain
W--> 133 <400> SEQUENCE: 11
        134 Gly Asn Thr Leu Ser Gln Asn Val
        135                 5           8
        137 <210> SEQ ID NO: 12
        138 <211> LENGTH: 26
        139 <212> TYPE: PRT
        140 <213> ORGANISM: Phage T4
W--> 141 <220> FEATURE:
        142 <221> NAME/KEY: DOMAIN
        143 <223> OTHER INFORMATION: the sixth coiled coil segment of the _-helical
        144       central domain of the fibritin
W--> 145 <400> SEQUENCE: 12
        146 Val Tyr Ser Arg Leu Asn Glu Ile Asp Thr Lys Gln Thr Thr Val
        147                 5                   10                  15
        148 Glu Ser Asp Ile Ser Ala Ile Lys Thr Ser Ile
        149                 20                  25
        151 <210> SEQ ID NO: 13
        152 <211> LENGTH: 361
        153 <212> TYPE: PRT
        154 <213> ORGANISM: artificial sequence
W--> 155 <220> FEATURE:
        156 <221> NAME/KEY: CHAIN
        157 <223> OTHER INFORMATION: the fiber-fibritin-6H chimera
W--> 158 <400> SEQUENCE: 13
        159 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr
        160                 5                   10                  15
```

```
161 Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr
162               20              ·         25              30
163 Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
164               35                        40              45
165 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly
166               50                        55              60
167 Met Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly
168               65                        70              75
169 Asn Leu Thr Ser Gln Asn Val Tyr Ser Arg Leu Asn Glu Ile Asp
170               80                        85              90
171 Thr Lys Gln Thr Thr Val Glu Ser Asp Ile Ser Ala Ile Lys Thr
172               95                        100             105
173 Ser Ile Gly Tyr Pro Gly Asn Asn Ser Ile Ile Thr Ser Val Asn
174               110                       115             120
175 Thr Asn Thr Asp Asn Ile Ala Ser Ile Asn Leu Glu Leu Asn Gln
176               125                       130             135
177 Ser Gly Gly Ile Lys Gln Arg Leu Thr Val Ile Glu Thr Ser Ile
178               140                       145             150
179 Gly Ser Asp Asp Ile Pro Ser Ser Ile Lys Gly Gln Ile Lys Asp
180               155                       160             165
181 Asn Thr Thr Ser Ile Glu Ser Leu Asn Gly Ile Val Gly Glu Asn
182               170                       175             180
183 Thr Ser Ser Gly Leu Arg Ala Asn Val Ser Trp Leu Asn Gln Ile
184               185                       190             195
185 Val Gly Thr Asp Ser Ser Gly Gly Gln Pro Ser Pro Pro Gly Ser
186               200                       205             210
187 Leu Leu Asn Arg Val Ser Thr Ile Glu Thr Ser Val Ser Gly Leu
188               215                       220             225
189 Asn Asn Asp Val Gln Asn Leu Gln Val Glu Ile Gly Asn Asn Ser
190               230     ·                 235             240
191 Thr Gly Ile Lys Gly Gln Val Val Ala Leu Asn Thr Leu Val Asn
192               245                       250             255
193 Gly Thr Asn Pro Asn Gly Ser Thr Val Glu Glu Arg Gly Leu Thr
194               260                       265             270
195 Asn Ser Ile Lys Ala Asn Glu Thr Asn Ile Ala Ser Val Thr Gln
196               275                       280             ·285
197 Glu Val Asn Thr Ala Lys Gly Asn Ile Ser Ser Leu Gln Gly Asp
198               290                       295             300
199 Val Gln Ala Leu Gln Glu Ala Gly Tyr Ile Pro Glu Ala Pro Arg
200     ·         305            ·          310             315
201 Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
202               320                       325             330
203 Ser Thr Phe Leu Ser Pro Ala Gly Gly Gly Gly Ser Gly Gly Gly
204               335                       340             345
205 Gly Ser Gly Gly Gly Gly Ser Arg Gly Ser His His His His His
206               350                       355             360
207 His
208 361
210 <210> SEQ ID NO: 14
```

```
      211 <211> LENGTH: 9
      212 <212> TYPE: PRT
      213 <213> ORGANISM: Unknown
W--> 214 <220> FEATURE:
      215 <221> NAME/KEY: DOMAIN
      216 <223> OTHER INFORMATION: a peptide ligand containing the RGD motif
W--> 217 <400> SEQUENCE: 14
      218 Cys Asp Cys Arg Gly Asp Cys Phe Cys
      219                  5               9
```

VERIFICATION SUMMARY   DATE: 05/09/2001
PATENT APPLICATION: US/09/612,852   TIME: 11:33:33

Input Set : **A:\09612852**
Output Set: **N:\CRF3\05092001\I612852.raw**

L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:11 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:13 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:
L:14 M:283 W: Missing Blank Line separator, <160> field identifier
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:32 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:48 M:283 W: Missing Blank Line separator, <400> field identifier
L:55 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:59 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:283 W: Missing Blank Line separator, <220> field identifier
L:68 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <220> field identifier
L:79 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:92 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:283 W: Missing Blank Line separator, <220> field identifier
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:102 M:283 W: Missing Blank Line separator, <400> field identifier
L:109 M:283 W: Missing Blank Line separator, <220> field identifier
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:119 M:283 W: Missing Blank Line separator, <220> field identifier
L:122 M:283 W: Missing Blank Line separator, <400> field identifier
L:129 M:283 W: Missing Blank Line separator, <220> field identifier
L:133 M:283 W: Missing Blank Line separator, <400> field identifier
L:141 M:283 W: Missing Blank Line separator, <220> field identifier
L:145 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:283 W: Missing Blank Line separator, <220> field identifier
L:158 M:283 W: Missing Blank Line separator, <400> field identifier
L:214 M:283 W: Missing Blank Line separator, <220> field identifier
L:217 M:283 W: Missing Blank Line separator, <400> field identifier